Metal stress response influences a soil bacterial community's permissiveness towards a broad-host-range plasmid

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Dominant clones of livers, spleens and fecal samples were whole genome sequenced to analyze for the presence o adaptive mutations. In one mouse a dominant clone from the fecal sample had a non-synonymous point mutation regulator of central carbon metabolism. In another mouse, dominant clones from both the liver and fecal sample h the same non-synonymous point mutation in a regulator of virulence gene expression. Interestingly, this clone was selected against in the spleen-sample from the same mouse. The contribution of these mutations to virulence and host-adaptation of Salmonella is presently being investigated. In conclusion, even during a short "chronic" infectio Salmonella undergoes genetic adaptation to its host. Furthermore, the genetic and host-niche specific nature of th mutations indicate that adjustment of central metabolism and virulence regulation involves niche-specific selectio

P2: Metal stress response influences a soil bacterial community's permissiveness towards a broad hos range plasmid

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The extent by which antibiotic resistance encoding plasmids transfer is of acute relevance in the age of massive antibiotic usage. The occurrence of stressors might play a major role in altering the acute permissiveness of a community towards plasmids, since plasmid transfer is considered a main process in immediate stress response an adaptation. A major stress factor for soil communities is the introduction of metals through geological or anthropogenic sources like manure.
We, therefore, aimed to assess how the introduction of metal stress alters a soil community's permissiveness towa plasmids. We also tried to evaluate if a general or a metal specific stress response exists.

Hence, using a ^{3}H-leucine-incorporation approach, we measured 25% and 50% inhibition concentrations for 5 meta (Cu, Zn, Ni, Cd, As). A mCherry-tagged *E. coli* donor carrying the *gfp*-tagged plasmid pKJK5 was mated with a soil bacterial community and exposed to metal stress. Plasmid transfer was quantified by detecting green fluorescent transconjugants. Transconjugants were isolated using fluorescent activated cell sorting. Sorted transconjugants we analyzed by 16S rRNA gene amplicon pyrosequencing. Within all transconjugal pools a high diversity of transconjugants remained irrespective of stress exposure. Still, results revealed an effect in soil microbial communi permissiveness towards broad-host-range plasmids when exposed to the heavy metals Ni or Cu, while As exposure showed no effect.

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